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RAW SEQUENCE LISTING   DATE: 02/26/2002
PATENT APPLICATION: US/09/908,988B   TIME: 14:06:37

        Input Set : A:\MYOG028.txt
        Output Set: N:\CRF3\02262002\I908988B.raw

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   3 <110> APPLICANT: OLSON, ERIC
   4        SPENCER, JEFFREY A.
   6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
   7        IN STRIATED MUSCLE CELLS
   9 <130> FILE REFERENCE: MYOG:028US
  11 <140> CURRENT APPLICATION NUMBER: 09/908,988B
C--> 12 <141> CURRENT FILING DATE: 2000-07-18
  14 <150> PRIOR APPLICATION NUMBER: 60/219,020
  15 <151> PRIOR FILING DATE: 2000-07-18
  17 <160> NUMBER OF SEQ ID NOS: 6
  19 <170> SOFTWARE: PatentIn Ver. 2.1
  21 <210> SEQ ID NO: 1
  22 <211> LENGTH: 1431
  23 <212> TYPE: DNA
  24 <213> ORGANISM: Mus musculus
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  27 <221> NAME/KEY: CDS
  28 <222> LOCATION: (199)..(1296)
  30 <400> SEQUENCE: 1
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  35 tgaccgagga agggtgcaca ggcaggggag aaggccaacg acagggccac agcgaggcag 180
  37 gctccagagc gccgcgggg atg aac ttc acg gtg ggt ttc aag ccg ctg cta 231
  38                          Met Asn Phe Thr Val Gly Phe Lys Pro Leu Leu
  39                           1               5                  10
  41 ggg gat gcg cac aac atg gac aac ttg gag aag cag ctc att tgc ccc 279
  42 Gly Asp Ala His Asn Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro
  43              15              20              25
  45 atc tgc ctg gag atg ttc tcc aag ccc gtg gtg atc ttg ccc tgc caa 327
  46 Ile Cys Leu Glu Met Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln
  47          30              35              40
  49 cac aac ctg tgc cgc aag tgt gcc aac gac gtc ttc cag gcc tct aat 375
  50 His Asn Leu Cys Arg Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn
  51      45              50              55
  53 cct ctg tgg caa tcc cgg ggc tcc aca acg gtg tct tca gga gga cgt 423
  54 Pro Leu Trp Gln Ser Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg
  55  60              65              70              75
  57 ttc cga tgc cca tct tgt agg cac gag gtt gtc ctg gac agg cat ggt 471
  58 Phe Arg Cys Pro Ser Cys Arg His Glu Val Val Leu Asp Arg His Gly
  59              80              85              90
  61 gtc tat ggc ctg cag cgg aac ctg cta gtg gag aac atc att gac atc 519
  62 Val Tyr Gly Leu Gln Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile
  63          95              100             105
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65  tac aag cag gag tcc tcc cgg cca ctg cac gcc aag gct gaa cag cac    567
66  Tyr Lys Gln Glu Ser Ser Arg Pro Leu His Ala Lys Ala Glu Gln His
67          110                 115                 120
69  ctc atg tgt gag gag cac gag gac gag aag atc aac atc tac tgc ctg    615
70  Leu Met Cys Glu Glu His Glu Asp Glu Lys Ile Asn Ile Tyr Cys Leu
71          125                 130                 135
73  agc tgc gag gtg ccc acc tgc tct ctc tgc aag gtt ttc ggc gcc cac    663
74  Ser Cys Glu Val Pro Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His
75  140                 145                 150                 155
77  aag gac tgt gag gtg gcc cct ctg ccc acc att tac aaa cgc cag aag    711
78  Lys Asp Cys Glu Val Ala Pro Leu Pro Thr Ile Tyr Lys Arg Gln Lys
79                  160                 165                 170
81  agt gag ctg agc gat ggc atc gcg atg ctg gtg gcg ggc aat gac cgt    759
82  Ser Glu Leu Ser Asp Gly Ile Ala Met Leu Val Ala Gly Asn Asp Arg
83                  175                 180                 185
85  gtg cag gca gtg atc acc cag atg gag gag gtg tgc cag acc att gag    807
86  Val Gln Ala Val Ile Thr Gln Met Glu Glu Val Cys Gln Thr Ile Glu
87          190                 195                 200
89  gac aac agc cgc aga cag aag caa ctg tta aac cag agg ttc gag acc    855
90  Asp Asn Ser Arg Arg Gln Lys Gln Leu Leu Asn Gln Arg Phe Glu Thr
91          205                 210                 215
93  ctg tgc gcg gtt ttg gag gag cgc aag ggc gaa ctg ctt caa gca ctg    903
94  Leu Cys Ala Val Leu Glu Glu Arg Lys Gly Glu Leu Leu Gln Ala Leu
95  220                 225                 230                 235
97  gcc cgg gag cag gag gag aag ttg cag cgc gtg cgg ggc ctc atc cgc    951
98  Ala Arg Glu Gln Glu Glu Lys Leu Gln Arg Val Arg Gly Leu Ile Arg
99                  240                 245                 250
101 cag tac gga gac cac ttg gag ggc tcc tca aag ctg gtg gag tcc gcc    999
102 Gln Tyr Gly Asp His Leu Glu Gly Ser Ser Lys Leu Val Glu Ser Ala
103                 255                 260                 265
105 atc cag tcc atg gag gag ccg cag atg gct ctc tac ctc cag cag gca   1047
106 Ile Gln Ser Met Glu Glu Pro Gln Met Ala Leu Tyr Leu Gln Gln Ala
107         270                 275                 280
109 aag gag ctg atc aac aag gtc ggg gca atg tcg aag gtg gag ctg gca   1095
110 Lys Glu Leu Ile Asn Lys Val Gly Ala Met Ser Lys Val Glu Leu Ala
111         285                 290                 295
113 gga cgg ccg gag cca ggc tat gag agc atg gag caa ttc tct gtg agc   1143
114 Gly Arg Pro Glu Pro Gly Tyr Glu Ser Met Glu Gln Phe Ser Val Ser
115 300                 305                 310                 315
117 gtg gag cac gtg gcc gaa atg ttg cga acc atc gac ttc cag ccg ggc   1191
118 Val Glu His Val Ala Glu Met Leu Arg Thr Ile Asp Phe Gln Pro Gly
119                 320                 325                 330
121 gcc gct ggg gat gaa gag gat gac gac atg gct ttg gat ggg gag gag   1239
122 Ala Ala Gly Asp Glu Glu Asp Asp Asp Met Ala Leu Asp Gly Glu Glu
123                 335                 340                 345
125 ggc aat gcg ggg ctg gag gag gag cgg ctg gac gtg cca gaa ggc tca   1287
126 Gly Asn Ala Gly Leu Glu Glu Glu Arg Leu Asp Val Pro Glu Gly Ser
127                 350                 355                 360
129 ggc ctg cac tgacccgact ctgatccaga gcgcacaccc gaagcgggag           1336
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130 Gly Leu His
131     365
133 ccaagggatg ctgaggatct gcgcagagac caccgcgcca ccaagctcgg cttcccgccc 1396
135 ccgggaaggt tctcaataaa ggactcaagt gtccc                            1431
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139 <211> LENGTH: 366
140 <212> TYPE: PRT
141 <213> ORGANISM: Mus musculus
143 <400> SEQUENCE: 2
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145   1               5                  10                  15
147 Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met
148             20                  25                  30
150 Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg
151         35                  40                  45
153 Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn Pro Leu Trp Gln Ser
154     50                  55                  60
156 Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg Phe Arg Cys Pro Ser
157 65                  70                  75                  80
159 Cys Arg His Glu Val Val Leu Asp Arg His Gly Val Tyr Gly Leu Gln
160             85                  90                  95
162 Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Ser
163             100                 105                 110
165 Ser Arg Pro Leu His Ala Lys Ala Glu Gln His Leu Met Cys Glu Glu
166         115                 120                 125
168 His Glu Asp Glu Lys Ile Asn Ile Tyr Cys Leu Ser Cys Glu Val Pro
169     130                 135                 140
171 Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp Cys Glu Val
172 145                 150                 155                 160
174 Ala Pro Leu Pro Thr Ile Tyr Lys Arg Gln Lys Ser Glu Leu Ser Asp
175             165                 170                 175
177 Gly Ile Ala Met Leu Val Ala Gly Asn Asp Arg Val Gln Ala Val Ile
178             180                 185                 190
180 Thr Gln Met Glu Glu Val Cys Gln Thr Ile Glu Asp Asn Ser Arg Arg
181         195                 200                 205
183 Gln Lys Gln Leu Leu Asn Gln Arg Phe Glu Thr Leu Cys Ala Val Leu
184     210                 215                 220
186 Glu Glu Arg Lys Gly Glu Leu Leu Gln Ala Leu Ala Arg Glu Gln Glu
187 225                 230                 235                 240
189 Glu Lys Leu Gln Arg Val Arg Gly Leu Ile Arg Gln Tyr Gly Asp His
190             245                 250                 255
192 Leu Glu Gly Ser Ser Lys Leu Val Glu Ser Ala Ile Gln Ser Met Glu
193             260                 265                 270
195 Glu Pro Gln Met Ala Leu Tyr Leu Gln Gln Ala Lys Glu Leu Ile Asn
196         275                 280                 285
198 Lys Val Gly Ala Met Ser Lys Val Glu Leu Ala Gly Arg Pro Glu Pro
199     290                 295                 300
201 Gly Tyr Glu Ser Met Glu Gln Phe Ser Val Ser Val Glu His Val Ala
202 305                 310                 315                 320
```

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204 Glu Met Leu Arg Thr Ile Asp Phe Gln Pro Gly Ala Ala Gly Asp Glu
205             325             330             335
207 Glu Asp Asp Asp Met Ala Leu Asp Gly Glu Glu Gly Asn Ala Gly Leu
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210 Glu Glu Glu Arg Leu Asp Val Pro Glu Gly Ser Gly Leu His
211     355             360             365
215 <210> SEQ ID NO: 3
216 <211> LENGTH: 2590
217 <212> TYPE: DNA
218 <213> ORGANISM: Mus musculus
220 <220> FEATURE:
221 <221> NAME/KEY: CDS
222 <222> LOCATION: (80)..(1714)
224 <400> SEQUENCE: 3
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227 ggacagggac ggcaaggaa atg agc act tct ctg aat tac aag tct ttc tcc 112
228                     Met Ser Thr Ser Leu Asn Tyr Lys Ser Phe Ser
229                      1               5                  10
231 aaa gag cag cag acc atg gat aac ttg gaa aag caa ctg atc tgt ccc 160
232 Lys Glu Gln Gln Thr Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro
233             15              20              25
235 atc tgc cta gag atg ttc acg aag cct gtg gtc att ctc cct tgc cag 208
236 Ile Cys Leu Glu Met Phe Thr Lys Pro Val Val Ile Leu Pro Cys Gln
237         30              35              40
239 cac aac ctg tgc agg aaa tgt gcc agt gac atc ttc cag gcc tct aac 256
240 His Asn Leu Cys Arg Lys Cys Ala Ser Asp Ile Phe Gln Ala Ser Asn
241     45              50              55
243 ccg tac tta ccc aca aga gga ggc acc acc gtg gca tca ggg ggc cgc 304
244 Pro Tyr Leu Pro Thr Arg Gly Gly Thr Thr Val Ala Ser Gly Gly Arg
245 60              65              70              75
247 ttc cgc tgt ccc tcc tgc aga cat gag gtg gtg tta gac aga cat ggg 352
248 Phe Arg Cys Pro Ser Cys Arg His Glu Val Val Leu Asp Arg His Gly
249             80              85              90
251 gtc tat gga ctg cag agg aac ctg ctc gtg gaa aac att att gat atc 400
252 Val Tyr Gly Leu Gln Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile
253             95              100             105
255 tac aag cag gaa tcc acc agg cca gaa aaa aaa ttg gac cag ccc atg 448
256 Tyr Lys Gln Glu Ser Thr Arg Pro Glu Lys Lys Leu Asp Gln Pro Met
257     110             115             120
259 tgt gaa gag cat gaa gag gaa cgc atc aac atc tat tgt ctg aac tgt 496
260 Cys Glu Glu His Glu Glu Glu Arg Ile Asn Ile Tyr Cys Leu Asn Cys
261     125             130             135
263 gaa gtg ccc acc tgt tcc ttg tgc aag gtt ttt ggc gcc cat aag gac 544
264 Glu Val Pro Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp
265 140             145             150             155
267 tgc cag gtg gct ccc ctg act cat gtg ttc cag agg cag aag tca gag 592
268 Cys Gln Val Ala Pro Leu Thr His Val Phe Gln Arg Gln Lys Ser Glu
269             160             165             170
271 ctc agt gat ggt att gct gta ctt gtg gga agc aac gat aga gtc cag 640
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272 Leu Ser Asp Gly Ile Ala Val Leu Val Gly Ser Asn Asp Arg Val Gln
273             175             180             185
275 ggt gtg atc agc cag ctg gag gac acc tgt aaa act att gag gag tgc     688
276 Gly Val Ile Ser Gln Leu Glu Asp Thr Cys Lys Thr Ile Glu Glu Cys
277         190             195             200
279 tgc aga aag cag aaa cag gac ctg tgt gag aaa ttt gat cac cta tac     736
280 Cys Arg Lys Gln Lys Gln Asp Leu Cys Glu Lys Phe Asp His Leu Tyr
281     205             210             215
283 ggc atc ctg gag gag agg aag act gaa atg acc caa gcc atc act cga     784
284 Gly Ile Leu Glu Glu Arg Lys Thr Glu Met Thr Gln Ala Ile Thr Arg
285 220             225             230             235
287 aca cag gag gag aaa ctg gaa cat gtc cga act ctt atc agg aag tat     832
288 Thr Gln Glu Glu Lys Leu Glu His Val Arg Thr Leu Ile Arg Lys Tyr
289             240             245             250
291 tcc gat cac ctg gag aac gta tcc aag ttg gtg gag tca gga atc cag     880
292 Ser Asp His Leu Glu Asn Val Ser Lys Leu Val Glu Ser Gly Ile Gln
293             255             260             265
295 ttc atg gat gag ccc gaa atg gca gta ttt ctg cag aat gcc aag acc     928
296 Phe Met Asp Glu Pro Glu Met Ala Val Phe Leu Gln Asn Ala Lys Thr
297         270             275             280
299 ctg ttg caa aag atc gtg gaa gca tca aag gcg ttt cag atg gag aaa     976
300 Leu Leu Gln Lys Ile Val Glu Ala Ser Lys Ala Phe Gln Met Glu Lys
301     285             290             295
303 cta gaa caa ggt tat gag atc atg agc aac ttc act gtc aat ctc aat    1024
304 Leu Glu Gln Gly Tyr Glu Ile Met Ser Asn Phe Thr Val Asn Leu Asn
305 300             305             310             315
307 aga gaa gaa aaa att atc cgt gaa att gac ttt tct aga gaa gag gaa    1072
308 Arg Glu Glu Lys Ile Ile Arg Glu Ile Asp Phe Ser Arg Glu Glu Glu
309             320             325             330
311 gag gaa gaa gat gca gga gaa ata gat gaa gaa gga gaa gga gag gat    1120
312 Glu Glu Glu Asp Ala Gly Glu Ile Asp Glu Glu Gly Glu Gly Glu Asp
313             335             340             345
315 gca gta gaa gta gaa gag gca gaa aat gtt caa ata gca tct tca ggg    1168
316 Ala Val Glu Val Glu Glu Ala Glu Asn Val Gln Ile Ala Ser Ser Gly
317         350             355             360
319 gaa gag gag agt ctg gag aaa gct gca gag ccc tct cag ctt ccc gca    1216
320 Glu Glu Glu Ser Leu Glu Lys Ala Ala Glu Pro Ser Gln Leu Pro Ala
321     365             370             375
323 gag ctt cag gtc gcc cca gag cca cta cct gct tcc tct cca gaa ccg    1264
324 Glu Leu Gln Val Ala Pro Glu Pro Leu Pro Ala Ser Ser Pro Glu Pro
325 380             385             390             395
327 ttt tca tcc atg cca cct gct gca gat gtc ctg gtg aca cag ggg gag    1312
328 Phe Ser Ser Met Pro Pro Ala Ala Asp Val Leu Val Thr Gln Gly Glu
329             400             405             410
331 gtg gtg ccc att ggc tct cag cag acc aca cag tct gaa act tca ggc    1360
332 Val Val Pro Ile Gly Ser Gln Gln Thr Thr Gln Ser Glu Thr Ser Gly
333             415             420             425
335 cct tca gca gcg gaa act gcg gat ccc ttg ttt tac cct agt tgg tat    1408
336 Pro Ser Ala Ala Glu Thr Ala Asp Pro Leu Phe Tyr Pro Ser Trp Tyr
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VERIFICATION SUMMARY   DATE: 02/26/2002
PATENT APPLICATION: US/09/908,988B   TIME: 14:06:39

Input Set : **A:\MYOG028.txt**
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date